QCI® Interpret One
Oncology variant interpretation just got more precise
Deliver oncologist-ready variant interpretation reports

Competing to offer an in-house comprehensive genomic profiling service for tumor samples is challenging, especially as panels increase in size and complexity. Today’s clinical labs are under mounting pressure to interpret next-generation sequencing (NGS) tests faster and with greater precision than ever before. That’s why we created QCI Interpret One.

With QCI Interpret One, lab directors can prepare, prioritize and report on clinically relevant variants associated with solid tumors and hematological malignancies without the time-consuming step of researching and writing variant- and disease-specific evidence summaries. Users get access to an “expert second opinion” for variant classification, and they can deliver professional reports directly to physicians and oncologists to better inform clinical decision making.

By combining automatable QIAGEN Clinical Insights software, powered by superior structured content in the QIAGEN Clinical Knowledge Base, with the trusted services of N-of-One, a QIAGEN company and world-leading provider of somatic variant interpretation, QCI Interpret One helps clinical labs advance their complex genomic profiling services to enable personalized cancer care.

Confidently interpret variants
In addition to expertly curated sources, such as professional guidelines, FDA therapies, clinical trials, and published literature, QCI Interpret One provides access to decision-ready oncologist-reviewed variant interpretive comments for confident decision-making.

Accelerate test turnaround time
Speed up variant interpretation with dynamically computed disease-specific variant classification, immediate access to interpretive comments, and automatable workflows to help you scale for higher test volumes.

Deliver oncologist-ready reports
Generate customizable and standardized clinical reports with variant- and disease-specific information, including molecular function, and diagnostic, prognostic, and therapeutic relevance, available treatments, and open and recruiting clinical trials.
Confident classifications for every variant, for every disease, for every patient

The content core of QCI Interpret One, the QIAGEN Clinical Knowledge Base transforms unstructured data into actionable insight. By aggregating, manually curating, and modeling scientific literature and professional guidelines with semantic consistency, the QIAGEN Clinical Knowledge Base captures biological, phenotypic, therapeutic, and outcomes information that enables QCI Interpret One to compute variant- and disease-specific classifications for every alteration in every disease for every patient case.

Over 200,000 tumors interpreted

New to QIAGEN Clinical Insights is the inclusion of oncologist-reviewed interpretative comments from N-of-One. With over a decade of experience in clinical genomics interpretation for oncology, N-of-One’s team has interpreted more than 200,000 tumor samples for pathologists and lab directors. Variant scientists and oncologists translate molecular data specific to each patient into state-of-the-art clinical insights within minutes, giving you immediate access to variant- and disease-specific expert summaries. Aggregated knowledge from N-of-One experts and the QIAGEN Clinical Knowledge Base allows you to confidently classify variants and better determine their clinical significance.

Superior structured content

The QIAGEN Clinical Knowledge Base delivers superior structured content directly to your variant interpretation pipeline allowing you to instantly prioritize variants and dynamically review the clinical relevance based on the phenotype. For every variant in over 31,000 cancer types, you receive a computed ACMG and AMP classification, computed molecular function, the alteration’s incidence in disease, structured interpretative comments, information on hereditary clinical cases, treatment information, including alteration-specific drug sensitivity and resistance, and a list of open and recruiting clinical trials. All the information you need is in one location, saving you time and money.

Sample of an oncology interpretation summary customizable with additional ready-to-use in-depth information on the diagnostic, prognostic, therapeutic significance and supporting study outcomes of relevant Phase 1-3 clinical studies and pre-clinical studies.

Through QCI Interpret One, you access:

- Oncologist-reviewed variant- and disease-specific interpretation summaries updated weekly
- >170,000 variant-specific expert molecular impact summaries updated weekly
- FDA approved therapeutics updated weekly
- Open and recruiting clinical trials updated weekly
- Professional guidelines (NCCN, ACMG, AMP/ASCO/CAP, WHO) updated weekly
- Curated bibliography of >300,000 variant-specific articles with hyperlinked citations for quick confirmation updated weekly
- >25 databases, including COSMIC, ClinVar, and population frequency database, such gnomAD and QIAGEN’s Allele Frequency Community (AFC)
- Therapeutic, prognostic, and diagnostic evidence, and clinical/functional studies updated weekly
Accelerate test turnaround time

QCI Interpret One enables clinical labs to speed up variant interpretation through automatable workflows and integrated curation and interpretation services.

Decision-ready interpretations at your fingertips

QCI Interpret One instantly delivers concise oncologist-reviewed evidence for each biomarker in the context of the cancer sub-type, listing information on the mutation’s molecular characteristics, roles in disease, and therapeutic, prognostic, and diagnostic implications. Saving you significant time by eliminating the need for manual curation and providing you with over 170,000 decision-ready interpretive comments for your reports, QCI Interpret One helps you accelerate test turnaround time and increase caseload volume.

Configurable and automatable workflows

With QCI Interpret One, you can reduce hands-on time with configurable and automatable NGS interpretation workflows. Plus, you can access preconfigured, ready-to-use workflows for commercial panels, such as Illumina TruSight Oncology 500, TruSight Tumor 170, and AmpliSeq Myeloid Panel. The software also lets you customize your lab’s specific reporting policies to automate variant reporting and drug and trial selection, and you can leverage a feature-rich API to integration with your LIMS to scale-up your case processing.

On-demand clinical curation and interpretation services

Leave the heavy-lifting to QIAGEN. On top of accessing over 170,000 decision-ready interpretive comments, you can submit your variants to QIAGEN to receive customized, oncologist-reviewed interpretations and summary comments for every clinically relevant variant detected. An ideal solution for labs working with rare or novel variants, QCI Interpret One’s on-demand clinical curation and interpretation services does the research, curation, and interpretation for you, replacing labor intensive processes with automated simplicity. Any somatic NGS panel can be submitted, and depending on size and complexity, results can be returned within hours.

VCF to report in three simple steps with QCI Interpret One

Instantly prioritize clinically relevant variants

Dynamically compute disease-specific variant classifications and drug and trial selection

Customized reporting

Access to variant- and disease-specific content
- Biological, prognostic, diagnostic, and therapeutic evidence
- Approved treatments and open/recruiting clinical trials
- Expert molecular function summaries

Expert decision-ready interpretations with oncologist-reviewed clinical evidence

We've got you covered.
Deliver oncologist-ready reports

The content, transparency, and delivery of clinical oncology NGS test reports are critical for timely and effective patient care. QCI Interpret One supports customizable and standardized reporting to ensure adherence with industry guidelines, while also making reports easy to understand and act upon by oncologists and clinicians.

QCI Interpret One is designed to augment in-house expertise. By providing you with all of the content necessary to generate a comprehensive, patient-specific report, yet giving you full control over final classifications, comments, and recommendations, the software and service enhance decision-making in the clinical workflow. With over 170,000 oncologist-reviewed variant- and disease-specific interpretive comments, AMP/ASCO/CAP and ACMG/AMP-based classifications, and customizable report components to support your unique panel, reporting policies, and customer need, QCI Interpret One enables professional, up-to-date clinical oncology reporting.

QCI Interpret One reports include:

- Oncologist-reviewed variant- and disease-specific interpretation summaries offering concise, intermediate, or comprehensive information on:
  - Molecular function
  - Therapeutic, prognostic, and diagnostic relevance
  - Variant interactions, such as effect of co-occurring variants on therapies, drug resistance and sensitivities
- Clinical practice guideline recommendations
- Relevant local recruiting clinical trials
- FDA-approved drug therapies
- Primary literature references
Deliver oncologist-ready reports in minutes with

1. Provide a panel description and include summary comments of test results.

2. Identify clinically significant variants with respect to potential treatments, variants with potential clinical significance and associated therapies, and variants with biological significance.

3. Notify oncologists of potential interactions.


5. Provide a Table of Contents to orient oncologists for fast review.

*This is a sample report that has been edited to illustrate key components.*
clinically actionable evidence and recommendations

GUIDELINES

The NCCN Guidelines (v.2.2020) note that Her2-positive breast carcinoma patients may consider adjuvant chemotherapy plus trastuzumab, regardless of hormone receptor status, depending on the physician’s evaluation of the individual patient. In certain situations, regimens including pertuzumab, ado-trastuzumab emtansine, or lapatinib may also be considered. The NCCN Guidelines (v.3.2020) list fulvestrant plus alpelisib as a preferred second-line therapy (category 1) for hormone receptor-positive, HER2-negative breast cancer patients with tumors harboring a PI3KCA mutation.

INTERACTIONS

PI3K pathway activation, as evidenced by the presence of activating PI3KCA mutations or decreased expression of Pho, has been associated with resistance to HER2-targeted therapies in some clinical studies, though in other studies no association was found [Guzman et al., 2015; 2022G6275, Desou et al., 2016; 20509680, Majewski et al., 2015; 20559818, Pature-Gale et al., 2015; 20559816, Chandrapalapiyi et al., 2012; 20559814, Dutta et al., 2014; 20559813, Pham et al., 2022G6275, Pham.20559818, Pham.20559816, Pham.20592874, Pham.20559813].

TREATMENT OPTIONS

- **Therapies with potential clinical benefit**:
  - **DS8201A**
    - Fam-trastuzumab deruxtuzumab, a HER2-directed antibody and topoisomerase inhibitor conjugate, is FDA-approved for treating adult patients with untreated or metastatic HER2-positive breast cancer who have received two or more prior HER2-directed regimens in the metastatic setting.

- **Available Clinical Trials**
  - **Phase 3 clinical trials**:
    - **TRASTUZUMAB EMTANSINE, TUCATINIB**
      - Randomized, Double-Blind, Phase 3 Study of Tucatinib or Placebo in Combination With Ado-trastuzumab Emtansine (T-DM1) for Subjects With Unresectable Locally-Advanced or Metastatic HER2+ Breast Cancer (HER2CLIMB-02)
      - NCT03797942
      - **Contact**: United States: AZ, CA, CO, DE, FL, GA, IL, MI, MD, MO, NE, NJ, OR, TX, VA
      - **Seattle Genetics Trial Information Support**: clinicaltrials@SeattleGenetics.com

- **VARIANT DETAILS**
  - **PIK3CA H1047R**
    - **Gene**: PIK3CA
    - **Exon**: 21
    - **Nucleotide**: NM_005321.4:g.71880239A>G, c.3140A>G
    - **Amino Acid**: p.H1047R
    - **Allelic Fraction**: 32.0% (of 2977 reads)
    - **Classification**: Tier 1A
    - **Assessment**: Pathogenic
    - **Treatment options**: 1 Sensitive, 10 Trials

- **Biomarker summary**: PIK3CA-H1047R is an activating mutation.
  - **Clinical relevance**: PIK3CA encodes the protein p110alpha, which is the catalytic subunit of phosphatidylinositol 3-kinase (PI3K). The PI3K pathway is involved in cell signaling that regulates a number of critical cellular functions, including cell growth, proliferation, differentiation, motility, and survival [169, 166]. Activating PIK3CA alterations may predict sensitivity to PI3K/Akt/mTOR pathway inhibitors, several of which are currently being tested in clinical trials [90, 132]. In addition, the p110alpha inhibitor alpelisib has been approved by the FDA for the treatment of postmenopausal women, and men, with PIK3CA-mutated, hormone receptor-positive, HER2-negative advanced or metastatic breast cancer who experience disease progression on or following an endocrine-based therapy [8].

  - **Disease summary**: A study of 1394 early stage breast cancer samples reported that positive p110alpha expression was associated with higher tumor grade, larger tumor size, nodal involvement, and vascular invasion. Higher p110alpha-expression was associated with basal-like breast cancer, HER2-positive breast cancer, and triple-negative breast tumors [5]. Additional studies have reported that p110alpha-positivity is associated with lower grade disease in breast cancer samples [103, 133, 168]. A pooled analysis of 10319 breast cancer patients from 19 studies has reported that PIK3CA mutation was associated with ER positivity, lower tumor grade, and smaller tumor size [229]. PIK3CA mutations and activation of the PI3K pathway may play a role in resistance to hormonal therapy in ER-positive breast cancers, as well as to HER2-targeted therapies in HER2-positive breast cancers, although some studies have reported no association between activation of the PI3K pathway and resistance to HER2-targeted therapies [81, 83, 143, 158, 213, 17, 113].

  - **Molecular function**: PIK3CA H1047R is a missense alteration that occurs in the kinase domain of the p110alpha protein (UniProt: H1047R) is a commonly reported hotspot mutation in the PIK3CA gene, and has been reported to result in increased lipid binding, elevated kinase activity, and oncogenic transformation in preclinical studies [101, 81, 13, 88, 149].
Choose the clinical oncology NGS test interpretation solution that best fits your needs

QIAGEN Clinical Insights (QCI)
A clinical genomics interpretation portfolio offering expert-curated knowledge, software and services, QCI supports clinical NGS testing for any indication, on your platform, with unlimited scalability.

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Learn more about QCI Interpret One and the QCI portfolio at [www.digitalinsights.qiagen.com/qci-interpret-one](http://www.digitalinsights.qiagen.com/qci-interpret-one)

QCI Interpret One is an evidence-based decision support software and service intended as an aid in the interpretation of variants observed in genomic next-generation sequencing data. The software and service evaluates genomic variants in the context of published biomedical literature, professional association guidelines, publicly available databases, annotations, drug labels, and clinical trials. Based on this evaluation, the software proposes a classification and bibliographic references to aid in the interpretation of observed variants. The software and service is NOT intended as a primary diagnostic tool by physicians or to be used as a substitute for professional healthcare advice. Each laboratory is responsible for ensuring compliance with applicable international, national, and local clinical laboratory regulations and other specific accreditations requirements.

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